

SEQUENCE LISTING

- <110> Genentech, Inc.
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- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
<141> 2000-09-18
- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20594
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<211> 353

<212> PRT

<213> Homo sapiens

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```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

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```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

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```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
          85              90              95

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```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

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```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130              135              140

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Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
340 345 350

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<211> 379

<212> PRT

<213> Homo sapiens

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 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65				70				75				80				
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Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly	
				100					105				110			
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro	
				115					120				125			
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln	
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Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu	
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Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys	
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Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp	Leu	
				290					295				300			
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys	
				305					310				315			
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His	
				325					330				335			
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala	
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Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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agggagcagc gacagtgtgc agatgtggac gagtgtcac tagca 45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c 21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 7

taagtccggc acattacagg tc 22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 8

cccacgatgt atgaatgggtg gactttgtgt gactcctggt ttctgcatc 49

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<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

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 oligonucleotide probe

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<210> 10
 <211> 23
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 <213> Artificial Sequence

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<210> 11
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 <213> Homo sapiens

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<210> 12
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<212> PRT
<213> Homo sapiens
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      20              25              30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35              40              45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50              55              60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
  65              70              75              80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85              90              95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100              105              110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115              120              125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130              135              140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
  145              150              155              160

His Asp Pro Gly

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<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

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 <223> a, t, c or g

<220>
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 <222> (80)
 <223> a, t, c or g

<220>
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 <222> (94)
 <223> a, t, c or g

<220>
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 <222> (144)
 <223> a, t, c or g

<220>
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 <222> (188)
 <223> a, t, c or g

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<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

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24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15

ggcggatatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 19

tgctgtgcta ctccctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
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Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
195 200 205

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

cagtacgtga gggaccaggg cgccatga

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gccca 24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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 <221> modified_base
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 <223> a, t, c or g

<400> 26
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<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
 tccagtcatt ttgattttgc tgtttatddd ttttttcttt ttctttttcc caccacattg 240
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 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

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 600
 700
 800
 900
 1000

<210>	29
<211>	21
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cgctccccc gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agagggcgac 120


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<210> 34
<211> 915
<212> PRT
<213> Homo sapiens
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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
35 40 45

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65 70 75 80

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
100 105 110

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
130 135 140

Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
				165					170					175	

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225 230 235 240
 Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
 245 250 255
 Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
 260 265 270
 Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
 275 280 285
 Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
 290 295 300
 Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
 305 310 315 320
 Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
 325 330 335
 Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
 340 345 350
 Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn
 355 360 365
 Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
 370 375 380
 Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
 385 390 395 400
 Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
 405 410 415
 Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
 420 425 430
 Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
 435 440 445
 Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
 450 455 460
 Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
 465 470 475 480
 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
 485 490 495
 His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
 500 505 510

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 700
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Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
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 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
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 625 630 635 640
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 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
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 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
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 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
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 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
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 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
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 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
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 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
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 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

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Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
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Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

Arg Tyr Arg
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

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<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

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<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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tttgtatgaa aaa
1813

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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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			20					25					30						
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val				
			35					40					45						
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln				
			50					55					60						
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys				
			65		70						75					80			
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro				
					85					90					95				
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg				
			100					105					110						
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val				
			115					120					125						
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr				
			130		135						140								
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu				
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Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser				
			165					170					175						
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro				
			180					185					190						
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser				
			195					200					205						
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys				
			210		215						220								
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu				
225					230					235					240				
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly				
			245					250					255						
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His				
			260					265					270						
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp				
			275		280						285								

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50

 <210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 43
 gtgtgacaca gcgtgggc 18

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 44
 gaccggcagg cttctgcg 18

 <210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 45
 cagcagcttc agccaccagg agtgg 25

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 46
 ctgagccgtg ggctgcagtc tcgc 24

 <210> 47

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggt 180
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
 caaactgcc a tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
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<212> PRT
<213> Homo sapiens
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Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys		
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 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
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 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
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 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
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 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
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 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
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 <213> Homo sapiens
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<210> 61
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<212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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acctgcgata tccaacagaa ttg

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<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67

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48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

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Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro	
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		420				425						430				
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Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu	
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625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
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 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
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 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255
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<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
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<400> 77
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 <210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 78
 gggaatagat gtgatctgat tgg 23

 <210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 79
 cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

 <210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 80
 agcaaccgcc tgaagctcat cc 22

 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 81
 aaggcgcggt gaaagatgta gacg 24

 <210> 82

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
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<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

oligonucleotide probe

<400> 87

cctagcacag tgacgagggga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89

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50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
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 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
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Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
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 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
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 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
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 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence
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<400> 98
tgaccagtgg ggaaggacag 20
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```
<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<400> 99
acagagcaga ggggtgccttg
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```
<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<400> 100
tcaggqacaa gtgggtgtctc tccc 24

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<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 101
tcaggggaagg agtgtgcagt tctg 24

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<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 102
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<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
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<400> 103

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<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

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Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

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Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

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Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360				365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390					395					400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
			405						410					415	

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

F00120-106200

<213> Homo sapiens

<400> 108

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tgttcaccac atccccacac cccattgcca cttattttatt catctcagga aataaagaaa 1800
ggtcttgga agttaaaaa aaaaaaaaa aaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg 65	Asp	Asn	Phe	Gly	Gly 70	Gly	Asn	Thr	Ala	Trp 75	Glu	Glu	Glu	Asn	Leu 80
Ser	Lys	Tyr	Lys	Asp 85	Ser	Glu	Thr	Arg	Leu 90	Val	Glu	Val	Leu	Glu 95	Gly
Val	Cys	Ser	Lys 100	Ser	Asp	Phe	Glu	Cys 105	His	Arg	Leu	Leu	Glu 110	Leu	Ser
Glu	Glu	Leu 115	Val	Glu	Ser	Trp	Trp 120	Phe	His	Lys	Gln	Gln 125	Glu	Ala	Pro
Asp	Leu 130	Phe	Gln	Trp	Leu	Cys 135	Ser	Asp	Ser	Leu	Lys 140	Leu	Cys	Cys	Pro
Ala 145	Gly	Thr	Phe	Gly	Pro 150	Ser	Cys	Leu	Pro	Cys 155	Pro	Gly	Gly	Thr	Glu 160
Arg	Pro	Cys	Gly	Gly 165	Tyr	Gly	Gln	Cys 170	Glu	Gly	Glu	Gly	Thr	Arg 175	Gly
Gly	Ser	Gly	His 180	Cys	Asp	Cys	Gln	Ala 185	Gly	Tyr	Gly	Gly	Glu 190	Ala	Cys
Gly	Gln	Cys 195	Gly	Leu	Gly	Tyr	Phe 200	Glu	Ala	Glu	Arg	Asn 205	Ala	Ser	His
Leu	Val 210	Cys	Ser	Ala	Cys	Phe 215	Gly	Pro	Cys	Ala	Arg 220	Cys	Ser	Gly	Pro
Glu 225	Glu	Ser	Asn	Cys	Leu 230	Gln	Cys	Lys	Lys	Gly 235	Trp	Ala	Leu	His 240	His
Leu	Lys	Cys	Val	Asp 245	Ile	Asp	Glu	Cys	Gly 250	Thr	Glu	Gly	Ala	Asn 255	Cys
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Cys	Lys 290	Lys	Cys	Ser	Pro	Gly 295	Tyr	Gln	Gln	Val	Gly 300	Ser	Lys	Cys	Leu
Asp 305	Val	Asp	Glu	Cys	Glu 310	Thr	Glu	Val	Cys	Pro 315	Gly	Glu	Asn	Lys	Gln 320
Cys	Glu	Asn	Thr	Glu 325	Gly	Gly	Tyr	Arg	Cys 330	Ile	Cys	Ala	Glu	Gly 335	Tyr
Lys	Gln	Met	Glu 340	Gly	Ile	Cys	Val	Lys 345	Glu	Gln	Ile	Pro	Glu 350	Ser	Ala

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

110-113-50-22-22

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
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 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
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 aaagtcctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

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100

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<400> 118
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ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
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aatcctgtga agttgtcctg tgccactcgt ggctttttctt ctccccgtgt ggagtgggaag 240
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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10              15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85              90              95

```

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<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 120
tcgcggagct gtgttctgtt tccc

<210> 121
<211> 50
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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcgat ggggacaaag ggcgaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125

actcagcagt ggtaggaaag

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

```

cagcgcgtgg cccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcagggtt 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120
gcctggaggc cgcgcgcgag ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgcacagg gacttggact gcagcgatgg cagcgatgag gaggagtga 300
ggattgagcc atgtacccag aaagggcaat gccaccgcc ccctggcctc ccctgcccc 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccc 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tgggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gacgcctcc gccactggg gttactggtg gccatgaagg 840
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tcctgcagaa gtggccctgg agattgaggg tcctgggaca ctccctatgg agatccgggg 1080
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact cctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc                                     1210

```

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1             5             10             15

```

```

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
          20             25             30

```

```

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
          35             40             45

```

```

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
          50             55             60

```

```

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
          65             70             75             80

```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
 cccacgcgtc cggctctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
 gggtttagact ggcgggggga ggaggcggag gaggggaagg agctgcatgc atgagaccca 120
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccaga 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
 gattcaagct gaaggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
 atgaaggatt caagatccgg taccocgacc tacacaatat ggtttcatta tgtcgcgatg 660
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
 atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
 ctccaatggt gagtcacgga gatttcgtct gccaccgcg gccttggtgag cgctacaacc 960
 acggaactgt ggtggagttt tactgcgac cttggctacag cctcaccagc gactacaagt 1020
 acatcacctg ccagtatgga gagtgggttc cttcttatca agtctactgc atcaaatcag 1080
 agcaaactgt gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140


```
<210> 132
<211> 490
<212> PRT
<213> Homo sapiens
```

<400> 132															
Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5					10					15	
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
			20					25					30		
Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
		35					40					45			
Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
	50					55					60				
Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65					70					75					80
Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
				85					90					95	
Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
			100					105					110		
Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
		115					120					125			
Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
	130					135					140				
Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145					150					155					160
Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
				165					170					175	
Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn

			180				185				190				
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200					205			
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
		210					215					220			
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230					235					
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245					250					255	
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
				260					265					270	
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
		275					280					285			
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
		290					295					300			
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
				325					330					335	
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
				340					345					350	
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
				355					360					365	
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
		370					375					380			
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
				405							410			415	
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
				420					425					430	
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
		435							440					445	
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
		450					455					460			

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133
 atctcctatc gctgctttcc cgg 23

<210> 134
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
 agccaggatc gcagtaaaac tcc 23

<210> 135
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
 atttaaacctt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136
 <211> 1815
 <212> DNA
 <213> Homo sapiens

<400> 136
 cccacgcgtc cgtccgcgc cctccccccc gcctcccgtg cggtcgcgtg gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggctgcctgc 240
 tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

CCGCCTGCTG

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600
gcgagggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
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cagaccctag caciaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
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tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
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aaatgtcact tgggttggtg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaataaaag 1800
agcaggaaaa aaaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<210> 138

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaaggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccgggcgc cgcagaagac 120
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctgcg tggcgacttg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 ccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcggtc 660
 cactaacatt ttccggaatc tggagtccac ccgttggttg ctggctgggc ttttcagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
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attcctccac atcctagaga gcaacctgct gaaagccatg gactctgccca ctgccccga 1140
caagatcaga aagctgtatc tctatgctgc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
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ggtgccgaga ggttgccctg atgggctctg cccgctggac atgtttctga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

```

```
<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence
```


<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agtcatac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
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agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cctttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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acggaatttt aaggataaat tttctgaatt gggtatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

```
<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
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 gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggtcggctg 180
 cctgggcgctc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcgccac ctgagggtg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
 tgctctaacg aaagcactcc tgcctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
 gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840
 ggatggatct aggtatggag ttatggacac caccacagcc caggggccgaa gccctgtgga 900
 ggtggcccaag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
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gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggcccaac ttgtttattg cagcttataa tgggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1                      5                      10          15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20                      25          30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35                      40          45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
  50                      55          60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
  65                      70          75          80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85                      90          95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
          100                     105          110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115                     120          125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130                     135          140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145                     150          155          160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165                     170          175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180                     185          190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195                     200          205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

1140 1200 1260 1320 1380 1427

210 215 220
 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
 225 230 235 240
 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
 245 250 255
 Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270
 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285
 Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
 290 295 300
 Arg Lys Ser Lys Asn Ser
 305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
tcataactgtt ccatactcggc acgc

24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157
aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacacccaaa cgctcgagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccggttac tgatcgctctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcggtctg attacaggag ctgggcatgg 240
aattggggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
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gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggtgtag tctatacatc 480
agatttgctt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctgggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840
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aacattggaa aggatccttc ctgagcgctt cctggcagtt ttaaaacgaa aaatcagtgt 960
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gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

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<400> 159
Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
  1          5          10          15
Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
      20          25          30
Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
      35          40          45
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
      50          55          60
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
      65          70          75          80
Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
      85          90          95
Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
      100          105          110
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
      115          120          125
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130          135          140
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
      145          150          155          160
Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
      165          170          175
Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180          185          190
Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
      195          200          205
Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
      210          215          220
Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
      225          230          235          240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
      245          250          255

```



```
cccacgcgctc cgcggaacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120
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attgtttcgc tggctcctggt gatgcctggc cccctgtgatg ggctgtttcg ctccctatac 180
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctggccc tttcccagga 300
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 ttcttctgggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
 cagggtgggc cgggaggttc atccatgttt ggactctttg tggaaacatgg gccttatggt 480
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
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 gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
 atatttctctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
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 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
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 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980
 ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70					75				80	
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230					235						240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245				250						255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260				265						270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275						280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgcc cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tgcatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctgggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

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cgagggccttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atTTTTccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
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tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

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Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1             5             10             15

```

```

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20             25             30

```

```

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45

```

```

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60

```

```

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80

```

```

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95

```

```

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110

```

```

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115            120            125

```

```

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130            135            140

```

```

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145            150            155            160

```

```

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165            170            175

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Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
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 260 265 270
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 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
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 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
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 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
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 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

180 185 190
 195 200 205
 210 215 220
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 245 250 255
 260 265 270
 275 280 285
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 325 330 335
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 370 375 380
 385 390 395 400
 405 410 415
 420 425 430
 435 440 445

450 455 460
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
 465 470 475 480
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
 485 490 495
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
 500 505 510
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
 515 520 525
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
 530 535 540
 Leu Tyr Phe Leu Gly Glu Gln Arg
 545 550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

cttctgcctt ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

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<221> modified_base
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<223> a, t, c or g

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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
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```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20              25              30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35              40              45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50              55              60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65              70              75              80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85              90              95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100              105              110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115              120              125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130              135              140

```


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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
 50 55 60

Asp 65	Arg	Leu	Leu	Lys	Met 70	Arg	Trp	Ser	Gly	Leu 75	Asn	Ala	Ile	Gln	Phe 80
Tyr	Val	Pro	Trp	Asn 85	Tyr	His	Glu	Pro	Gln 90	Pro	Gly	Val	Tyr	Asn 95	Phe
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Glu 130	Met	Gly	Gly	Leu	Pro	Ser 135	Trp	Leu	Leu	Arg	Lys 140	Pro	Glu	Ile	His
Leu 145	Arg	Thr	Ser	Asp 150	Pro	Asp	Phe	Leu	Ala	Ala 155	Val	Asp	Ser	Trp	Phe 160
Lys	Val	Leu	Leu	Pro 165	Lys	Ile	Tyr	Pro	Trp 170	Leu	Tyr	His	Asn 175	Gly	Gly
Asn	Ile	Ile	Ser 180	Ile	Gln	Val	Glu	Asn 185	Glu	Tyr	Gly	Ser	Tyr 190	Arg	Ala
Cys	Asp	Phe 195	Ser	Tyr	Met	Arg	His 200	Leu	Ala	Gly	Leu	Phe 205	Arg	Ala	Leu
Leu 210	Gly	Glu	Lys	Ile	Leu	Leu 215	Phe	Thr	Thr	Asp	Gly 220	Pro	Glu	Gly	Leu
Lys 225	Cys	Gly	Ser	Leu	Arg 230	Gly	Leu	Tyr	Thr	Thr 235	Val	Asp	Phe	Gly	Pro 240
Ala	Asp	Asn	Met	Thr 245	Lys	Ile	Phe	Thr	Leu 250	Leu	Arg	Lys	Tyr 255	Glu	Pro
His	Gly	Pro	Leu 260	Val	Asn	Ser	Glu 265	Tyr	Tyr	Thr	Gly	Trp	Leu 270	Asp	Tyr
Trp	Gly	Gln 275	Asn	His	Ser	Thr	Arg 280	Ser	Val	Ser	Ala	Val 285	Thr	Lys	Gly
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Arg	Phe	Leu	Pro	Ile 325	Thr	Thr	Ser	Tyr	Asp 330	Tyr	Asp	Ala	Pro	Ile 335	Ser
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<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcaccag aatggtgttg gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
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<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
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 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
 tgcagcattt gcatactact gggaacaaag tggacattct gccaaaacaa ttgtttaaat 1320

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gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaag 1380
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agggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
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<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
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Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

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Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85             90             95

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```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100            105            110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115            120            125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130            135            140

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```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145            150            155            160

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```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165            170            175

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```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180            185            190

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Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
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 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
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 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

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<400> 189
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aaqacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctccctg 180
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atcgctgggtg gtatcctggc gcccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
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cacaaccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480
tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600
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agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys
290						295				300					
Asp	Pro	Thr	Cys	Arg	Pro	Lys	Leu	Ser	Asn	Val	Val	Glu	Phe	Ser	Val
305				310						315				320	
Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile
				325				330						335	
Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val
		340						345				350			
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly
		355				360						365			
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile
370						375				380					
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe
385				390						395				400	
Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val
				405				410						415	
Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp
		420						425				430			
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser
		435				440						445			
Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg
450						455				460					
Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe
465				470						475				480	
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu
				485				490						495	
Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys
		500						505				510			
Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys
		515				520						525			
Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg
530						535				540					
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu
545				550						555				560	
Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val	His	Leu	Phe	Ser	Phe	Met	Val

565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g 21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
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ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacctgg 180

gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240
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 ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaaacttta 2280
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 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe
50						55					60				
Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys
65					70					75					80
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro
				85					90					95	
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe
			100					105					110		
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr
		115					120					125			
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser
	130					135					140				
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp
145					150					155					160
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg
				165					170					175	
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu
			180					185					190		
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
		195					200					205			
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val
	210					215					220				
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser
225					230					235					240
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr
				245					250					255	
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly
			260					265					270		
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro
		275					280					285			
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr
	290					295					300				
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val
305					310					315					320
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn
				325					330					335	

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196
 tggtttgacc aggccaaagtt cgg

23

<210> 197
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197
 ggattcatcc tcaaggaaga gcgg

24

<210> 198

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gttccagaac	tctccatccg	gactagttat	tgagcatctg	cctctcatat	caccagtggc	120	
catctgaggt	gtttccctgg	ctctgaaggg	gtaggcacga	tggccaggtg	cttcagcctg	180	
gtgttgcttc	tcacttccat	ctggaccacg	aggctcctgg	tccaaggctc	tttgcggtga	240	
gaagagcttt	ccatccaggt	gtcatgcaga	attatgggga	tcacccttgt	gagcaaaaag	300	
gcgaaccagc	agctgaattt	cacagaagct	aaggaggcct	gtaggctgtg	gggcaataagt	360	
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tgttacaact	cattgtgatac	ttggactaac	tcgtgcattc	cagaaattat	caccaccaa	600	
gatcccatat	tcaacactca	aactgcaaca	caaacaacag	aatttattgt	cagtgcagct	660	
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gccaatgata	gcaaccctaa	tgaggaatca	aagaaaactg	ataaaaacc	agaagagtcc	1080	
aagagtccaa	gcaaaactac	cgtgcgatgc	ctggaagctg	aagtttagat	gagacgaaa	1140	
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cctgctctgga	tcctatcctc	ctacctccaa	agcttcccac	ggcctttcta	gcctggctat	1380	
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<210> 201
<211> 322
<212> PRT
<213> Artificial sequence
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<400> 201																
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			20					25					30			
Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	
		35					40					45				
Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu	
	50					55					60					
Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	
65					70					75					80	
Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	
				85					90					95		
Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	
			100					105					110			
Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	
		115					120					125				
Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile	
	130					135					140					

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

22

24

50

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<220>
<221> modified base
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<222> (1003)

<223> a, t, c or g

<400> 206

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ggctcgccca accttactac cttctgtcgg ccttgccttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacgggtctgc ccaccaacg cgaagacggt aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaaat tcttttcttc cgcttggata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccoc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggtc acttggattg 480
tggagtctct tgccaattgg tctaataact gccaatcatt tgcccttacc tatgctgacc 540
tctcccttaa atacaactgt acaggggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgagca catcacccct caccaagcaa ctccctaccc 660
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tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gacgagcctg 840
tggttcaac cccaccacaa gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gtgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
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actttccttt gtgtggtagg acttgaggga gaaatccctt ggactttcac taacctctg 1560
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```

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1              5              10              15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65              70              75              80

```


Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285
 Asp Gly Glu Asn Lys Lys Asp Lys
 290 295
 <210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 208
 gcttgatata tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60
 tggggcccca gcctggcccg ggtaaccctg gcatgaggag atgggcctgt tgctcctggg 120
 cccattgctc ctgctgcccg gctcctacgg actgcccttc tacaacggct tctactactc 180
 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
 cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcggtg tgcgtgtcaa 360
 atgggtggaag ctgtcggaga acggggcccc agagaaggac gtgctgggtg ccatcgggct 420
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
 ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtggt 600

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<210> 213
<211> 360
<212> PRT
<213> Homo sapiens
```

```

<400> 213
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                               5                10                15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
  20                25                30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
  35                40                45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50                55                60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
  65                70                75                80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
  85                90                95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
  100                105                110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

```
<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
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<400> 214

18

<211> 18

<213> Artificial Sequence

<400> 215

18

<211> 18

<213> Artificial Sequence

<400> 216

18

<211> 18

<213> Artificial Sequence

<400> 217

18

<211> 24

<213> Artificial Sequence

<400> 218

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 219
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
 ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
 gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
 ccaactcacc ccagagga aa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300
 gcagcagcgg ggcgacggct ggggtgtcgt ggcgagctt cgcgcgtgga tcgcgcacac 360
 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
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 gcggcgcttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600
 agccttcctg caccocgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660
 ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggatct 720
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840
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 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly
			20						25			30			
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala
			35						40			45			
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val
			50			55						60			
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu
65			70						75			80			
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp
			85						90			95			
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg
			100						105			110			
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp
			115			120						125			
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly
130						135						140			
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr
145			150						155			160			
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp
			165						170			175			
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu
			180			185						190			
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr
195						200						205			
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu
210						215			220						
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala
225			230						235			240			
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn
			245						250			255			
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro
			260			265						270			
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu
275						280						285			

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gccacgga actt

44

<210> 226
 <211> 2403

<212> DNA

<213> Homo sapiens

<400> 226
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 tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140
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 tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gatttcacag 1980
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<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
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Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
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Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
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Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
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Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
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Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
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Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
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Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
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Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
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Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
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 305 310 315 320
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
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 370 375 380
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 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
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 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
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oligonucleotide probe

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18

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<211> 18

<212> DNA

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<223> Description of Artificial Sequence: Synthetic
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18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<400> 230

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18

<210> 231

<211> 18

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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180720-20230301

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<223> Description of Artificial Sequence: Synthetic
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<223> Description of Artificial Sequence: Synthetic
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 <213> Homo sapiens

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 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
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<210> 237

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<400> 237
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<400> 238
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<210> 239
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<400> 239
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<210> 240
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<400> 240
 ttggcagctt catggagg 18

<210> 241
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cactctcctt cctctccaaa cacacatgtg catgtacaca cacacataca 150
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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150

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Table 1. *Continued*

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Thr	Pro	Ala	His	Ala 470	Gly	Arg	Arg	Tyr	Arg 475	Val	Tyr	Pro	Glu	Gly 480
Thr	Leu	Glu	Leu	Arg 485	Arg	Val	Thr	Ala	Glu 490	Glu	Ala	Gly	Leu	Tyr 495
Thr	Cys	Val	Ala	Gln 500	Asn	Leu	Val	Gly	Ala 505	Asp	Thr	Lys	Thr	Val 510
Ser	Val	Val	Val	Gly 515	Arg	Ala	Leu	Leu	Gln 520	Pro	Gly	Arg	Asp	Glu 525
Gly	Gln	Gly	Leu	Glu 530	Leu	Arg	Val	Gln	Glu 535	Thr	His	Pro	Tyr	His 540
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Leu	Thr	Trp	Ser	Ser 560	Ala	Ser	Ser	Leu	Arg 565	Gly	Gln	Gly	Ala	Thr 570
Ala	Leu	Ala	Arg	Leu 575	Pro	Arg	Gly	Thr	His 580	Ser	Tyr	Asn	Ile	Thr 585
Arg	Leu	Leu	Gln	Ala 590	Thr	Glu	Tyr	Trp	Ala 595	Cys	Leu	Gln	Val	Ala 600
Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
Leu	Ile	Ala	Ile	Leu 635	Ala	Leu	Ala	Val	Leu 640	Leu	Leu	Ala	Ala	Gly 645
Leu	Ala	Ala	His	Leu 650	Gly	Thr	Gly	Gln	Pro 655	Arg	Lys	Gly	Val	Gly 660
Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
680 685 690

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<223> Synthetic Oligonucleotide Probe

<400> 246

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<211> 24

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<400> 247

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<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

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 aactcccga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850
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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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			20						25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

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				95					100					105
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
				110					115					120
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
				125					130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
				140					145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
				155					160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp
				230					235					240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu
				245					250					255
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr
				260					265					270
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu
				275					280					285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr
				305					310					315
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr
				320					325					330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser
				335					340					345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn
				350					355					360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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<213> Artificial Sequence

<220>

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<400> 251

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<210> 252

<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<211> 47

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<211> 1650

<213> Homo Sapien

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gcgctctccc gtcgccgagg gggttgctgct gctgccgctg ctgctggggcc 100

tgaacgcagg agctgtcatt gactggccca caagggaggg caaggaagta 150

tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200

ttatgccacc aactcctgca agaacttctc agaactgccc ctggatcatgt 250

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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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			20					25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
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Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
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Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
				65					70					75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
				80					85					90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
				95					100					105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
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Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
				125					130					135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
				140					145					150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser
				155					160					165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
				170					175					180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
				185					190					195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
				200					205					210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
				215					220					225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
				230					235					240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys
				245					250					255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr
				260					265					270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser
				275					280					285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His
				290					295					300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
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440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
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				20					25					30
Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
				35					40					45
Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
				50					55					60
Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70					75
Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
				80					85					90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
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<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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				20					25					30
Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu
				35					40					45
Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg
				50					55					60
Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln
				65					70					75
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg
				80					85					90
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala
				95					100					105
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu
				110					115					120
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly
				125					130					135
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val
				140					145					150
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro
				155					160					165
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser
				170					175					180
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly
				185					190					195
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn
				200					205					210
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln
				215					220					225
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu
				230					235					240
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala
				245					250					255
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly
				260					265					270
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala
				275					280					285

Figure 1. The structure of the *hsp70* gene. The exons are numbered 1 to 5. The introns are numbered 1 to 4. The size of the exons and introns is indicated in base pairs (bp). The size of the gene is indicated in base pairs (bp). The size of the gene is indicated in base pairs (bp).

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<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien
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attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150
agtgcgcctt tacagtgcct cctggaaacc cacttggcct gcataccgcc 200
tcctgtgctg cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtggtca 300
taagggaact ccactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggagccgca cagagacgca ggtgggcatt 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
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caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
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<210> 261
<211> 383
<212> PRT
<213> Homo Sapien
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<400> 261
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  1                      5                      10                      15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro
                      20                      25                      30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
                      35                      40                      45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
                      50                      55                      60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
                      65                      70                      75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
                      80                      85                      90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile
                      95                      100                      105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
                      110                      115                      120

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Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

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ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
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ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350
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cgggtccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
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Arg Ser

<211> 24

<213> Art.

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<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaagggttg 19

<210> 266

<211> 24

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

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<400> 272
cagccctgcc acatgtgc 18

<210> 273
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<400> 273
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<210> 274
<211> 24
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<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 278
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<210> 279
<211> 24
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<400> 279
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<210> 280
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<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcocatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

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atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

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ccgctactgc tactgctggg ggccaccaca ggccccgttg gagccctcac 100

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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
				20					25					30
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
				35					40					45
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
				50					55					60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
				65					70					75
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
				80					85					90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
				95					100					105
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
				110					115					120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
				125					130					135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
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 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
 155 160 165
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
 200 205 210
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
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 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
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Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
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<210> 286
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 286
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<210> 287
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 287
 ctcatattgc acaccagtaa ttcg 24

<210> 288
 <211> 45
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 atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
 <211> 3662
 <212> DNA
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<211> 1059
<212> PRT
<213> Homo Sapien
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Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
                      20                      25                      30

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Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	
				50					55					60	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	
				65					70					75	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	
				80					85					90	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	
				95					100					105	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	
				110					115					120	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	
				125					130					135	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	
				140					145					150	
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	
				155					160					165	
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	
				170					175					180	
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	
				185					190					195	
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	
				200					205					210	
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	
				215					220					225	
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	
				230					235					240	
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	
				245					250					255	
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	
				260					265					270	
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
				275					280					285	
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	

				290					295					300
Leu	Lys	Thr	Leu	Asp 305	Leu	Lys	Asn	Asn	Glu 310	Ile	Ser	Trp	Thr	Ile 315
Glu	Asp	Met	Asn	Gly 320	Ala	Phe	Ser	Gly	Leu 325	Asp	Lys	Leu	Arg	Arg 330
Leu	Ile	Leu	Gln	Gly 335	Asn	Arg	Ile	Arg	Ser 340	Ile	Thr	Lys	Lys	Ala 345
Phe	Thr	Gly	Leu	Asp 350	Ala	Leu	Glu	His	Leu 355	Asp	Leu	Ser	Asp	Asn 360
Ala	Ile	Met	Ser	Leu 365	Gln	Gly	Asn	Ala	Phe 370	Ser	Gln	Met	Lys	Lys 375
Leu	Gln	Gln	Leu	His 380	Leu	Asn	Thr	Ser	Ser 385	Leu	Leu	Cys	Asp	Cys 390
Gln	Leu	Lys	Trp	Leu 395	Pro	Gln	Trp	Val	Ala 400	Glu	Asn	Asn	Phe	Gln 405
Ser	Phe	Val	Asn	Ala 410	Ser	Cys	Ala	His	Pro 415	Gln	Leu	Leu	Lys	Gly 420
Arg	Ser	Ile	Phe	Ala 425	Val	Ser	Pro	Asp	Gly 430	Phe	Val	Cys	Asp	Asp 435
Phe	Pro	Lys	Pro	Gln 440	Ile	Thr	Val	Gln	Pro 445	Glu	Thr	Gln	Ser	Ala 450
Ile	Lys	Gly	Ser	Asn 455	Leu	Ser	Phe	Ile	Cys 460	Ser	Ala	Ala	Ser	Ser 465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
				470					475					480
Leu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
Gly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510
Val	Glu	Phe	Ala	Ser 515	Glu	Gly	Lys	Tyr	Gln 520	Cys	Val	Ile	Ser	Asn 525
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	Val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540
Met	Leu	Pro	Ser	Phe 545	Thr	Lys	Thr	Pro	Met 550	Asp	Leu	Thr	Ile	Arg 555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560		565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575		580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590		595	600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605		610	615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620		625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635		640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650		655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665		670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680		685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695		700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710		715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725		730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740		745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755		760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770		775	780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785		790	795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800		805	810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
 1025 1030 1035
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
 1040 1045 1050
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
 1055

<210> 291

<211> 2906

<213> Homo Sapien

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tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300
ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
ggtgtggtgg tgttttctt tctttttgaa tttcccacia gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
tttgtgcta tgttgactaa aattgacgga taattgcagt tggatttttc 650
ttcatcaacc tctttttttt taaattttta ttccttttgg tatcaagatc 700
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gtgatcagtc tgaaatacaa ctgtttgaat tocagaagga ccaacaccag 800
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 cctgacatct gtatcttggg ttactccaaa tggaacagtc atgacacatg 2000
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 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350
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 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

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 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacia 2850
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 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly					
	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly					
	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg					
	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp					
	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln					
	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile					
	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val					
	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp					
	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His					
	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp					
	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys					
	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp					
	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro					
	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys					
	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn					
	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val					
	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp					
	410		415		420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
 425 430 435
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
 440 445 450
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
 470 475 480
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
 485 490 495
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
 500 505 510
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
 515 520 525
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
 530 535 540
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
 545 550 555
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
 560 565 570
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
 605 610 615
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
 620 625 630
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
 635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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aaa 4053

<211> 1119

<213> Homo Sapien

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

215	220	225
Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala	
230	235	240
Leu Lys Ser Leu Lys Met Gln Arg Asn	Gly Val Thr Lys Leu Met	
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn	Met Glu Ile Leu Gln Leu	
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr	Lys Gly Trp Leu Tyr Gly	
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu	Ser Gln Asn Ala Ile Asn	
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe	Cys Gln Lys Leu Ser Glu	
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser	Arg Leu Asp Asp Ser Ser	
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr	Leu His Ile Gly Asn Asn	
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala	Phe Arg Gly Leu Ser Ser	
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr Ile	
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg Arg	
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys Ala	
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His	Leu Asp Leu Ser Asp Asn	
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys Lys	
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser	Ser Leu Leu Cys Asp Cys	
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe Gln	
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His	Pro Gln Leu Leu Lys Gly	
470	475	480

Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				755										765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				770										780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				785										795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				800										810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				815										825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				830										840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				845										855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
				860										870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				875										885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				890										900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				905										915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				920										930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				935										945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				950										960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His
				965										975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp
				980										990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn
				995										1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
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ccgtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250

cggcgaggca ggagggctca tggtagagcaa ggaggccggc tgatctgcag 300

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gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

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<400> 311
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<210> 312
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<400> 312
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<210> 313
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<400> 313
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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
              35              40              45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
              50              55              60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
              65              70              75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
              80              85              90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
              95              100              105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
              110              115              120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
              125              130              135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
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Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
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Thr Arg Pro Thr Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro	
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365	370	375
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Lys Asp Asn Asp Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly	
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Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser					
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Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala					
	470		475		480
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<400> 317

ttgcacttgt aggacccacg tacg 24

<210> 318

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atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900
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gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100
atcactatth ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150
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<210> 320
<211> 450
<212> PRT
<213> Homo Sapien
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Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
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His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
                50                55              60

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Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

	320	325	330
Ala Gln Lys Gly	Lys Ser Leu Ser Pro	Leu Ala Ser Ile Thr	Gly
	335	340	345
Ile Ser Leu Phe	Leu Ile Ile Ser Met	Cys Leu Leu Phe Leu	Trp
	350	355	360
Lys Lys Tyr Gln	Pro Tyr Lys Val Ile	Lys Gln Lys Leu Glu	Gly
	365	370	375
Arg Pro Glu Thr	Glu Tyr Arg Lys Ala	Gln Thr Phe Ser Gly	His
	380	385	390
Glu Asp Ala Leu	Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala	Phe
	395	400	405
Pro Asp Val Ser	Gly Val Ser Arg Ile	Pro Ser Arg Ser Val	Pro
	410	415	420
Ala Ser Asp Cys	Val Ser Gly Gln Asp	Leu His Ser Thr Val	Tyr
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Glu Val Ile Gln	His Ile Pro Ala Gln	Gln Gln Asp His Pro	Glu
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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<223> Synthetic Oligonucleotide Probe

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<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
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accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
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aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
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<212> PRT

<213> Homo Sapien

<400> 325

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Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

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215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys	Val Glu Glu Glu Gln Glu	
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu	Glu Ala Glu Ser Lys Glu	
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn	Ala Ile Arg Gln Arg Ser	
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys	Ser	
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<210> 326

<211> 23

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

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tgcagggttc agtctagatt g 21

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<211> 45

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<213> Artificial Sequence

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<211> 2168

<212> DNA

<213> Homo Sapien

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acttcctct	gtgaccatga	aactctgggt	gtctgcattg	ctgatggcct	200
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caatgctgag	tgtggatgac	tgctttggga	tgggccgctc	ggcctacaat	700
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cctaccagaa aaaaaaaaa 2168

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<213> Homo Sapien

<400> 332

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Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met
20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
200 205 210

2168:gtttttatgg cattttctatc tattgtggct ttaccaaaaa ataaaatgtc

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
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Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
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<210> 333

<211> 18

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 336
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<210> 337

<211> 45

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<400> 337

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<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

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agacaggaca atcttcttgg ggatgctggc cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
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Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
                35                      40                      45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
                50                      55                      60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
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Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
                80                      85                      90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

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95					100					105				
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
				110					115					120
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
				125					130					135
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
				140					145					150
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
				155					160					165
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile
				170					175					180
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu
				185					190					195
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala
				200					205					210
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly
				215					220					225
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg
				230					235					240
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro
				245					250					255
Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly
				260					265					270
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu
				275					280					285
Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu
				290					295					300
Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr
				305					310					315
Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr
				320					325					330
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val
				335					340					345
Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu
				350					355					360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	
				365					370					375	
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	
				380					385					390	
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	
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Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	
				410					415					420	
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	
				425					430					435	
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	
				440					445					450	
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	
				455					460					465	
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	
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Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	
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Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	
				500					505					510	
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	
				515					520					525	
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	
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Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	
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Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	
				560					565					570	
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	
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Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	
				590					595					600	
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	
				605					610					615	
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	
				620					625					630	

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
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 Gln Glu Gln Ala Asn Ser Thr
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<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

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<210> 341
<211> 318
<212> PRT
<213> Homo Sapien
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				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260 265 270
 Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
 275 280 285
 Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
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 305 310 315
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 <213> Artificial Sequence
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 <210> 343
 <211> 18
 <212> DNA
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 <223> Synthetic Oligonucleotide Probe
 <400> 343
 ctggttcttc cttgcacg 18
 <210> 344
 <211> 28
 <212> DNA
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 <400> 344
 gcccaaatgc cctaaggcgg tatacccc 28
 <210> 345
 <211> 50
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<400> 350

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<210> 351

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<400> 351

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<210> 352

<211> 47

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<400> 352

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<400> 353

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<210> 354

<211> 48

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<400> 354

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<210> 355

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<210> 356
<211> 46
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<400> 356
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<210> 357
<211> 48
<212> DNA
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<400> 357
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<210> 358
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<210> 359
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<400> 359
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<210> 360
<211> 48
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<210> 362
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<400> 363
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<210> 364
<211> 47
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<400> 364

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<210> 365

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<400> 366

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<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<210> 368

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 369

<211> 48

<212> DNA

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<400> 369

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<211> 48

<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

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<400> 371

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<211> 47

<212> DNA

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<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 373

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<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

100120-20000000

<223> Synthetic Oligonucleotide Probe

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<211> 48

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<211> 997

<213> Homo Sapien

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agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150

tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcacatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350

gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400

tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450

gtggttatca actcacagga ggagcaggaa ttcctttcct acaaqaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccaggtt gtcgagggtc 550

agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600

gatgtagggg agcccaacaa catagctacc ctggaggact gtqccaccat 650

gagagactct tcaaacccaa qgcaaaattg gaatgatgta acctgtttcc 700

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<210> 377
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<212> PRT
<213> Homo Sapien
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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60
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Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
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Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
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Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
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Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
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Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
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Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
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